

# The Functional Evolution Analysis of *COP1*

## *COP1*功能及演化分析

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- Introduction of *AtCOP1* (背景介绍)
- Expression pattern of *AtCOP1* (表达模式)
- Structural and functional analysis (结构功能分析)
- Protein interaction network (互作网络)
- Phylogeny analysis (演化分析)

# Phenotypes of dark- and light-grown soy



- Skotomorphogenic developmental mode
- Photomorphogenic developmental mode

# *AtCOP1* (constitutively photomorphogenic 1)

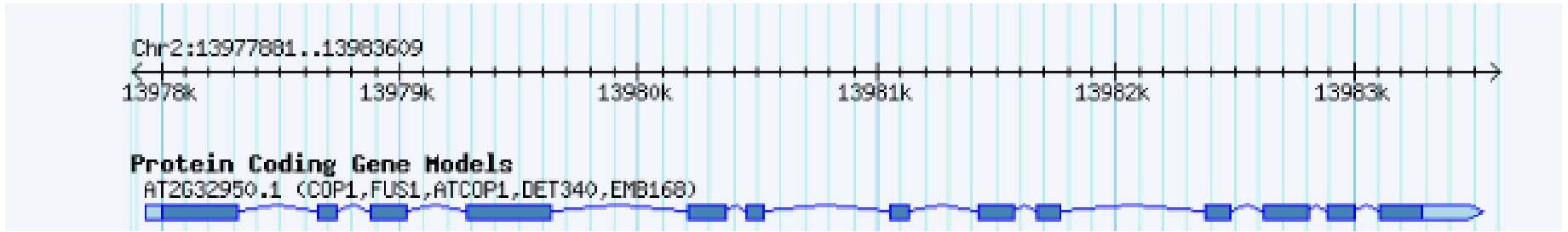


(Xing-Wang Deng, et al., Genes Dev, 1991)

**Seedlings were grown for 6 days from germination.**

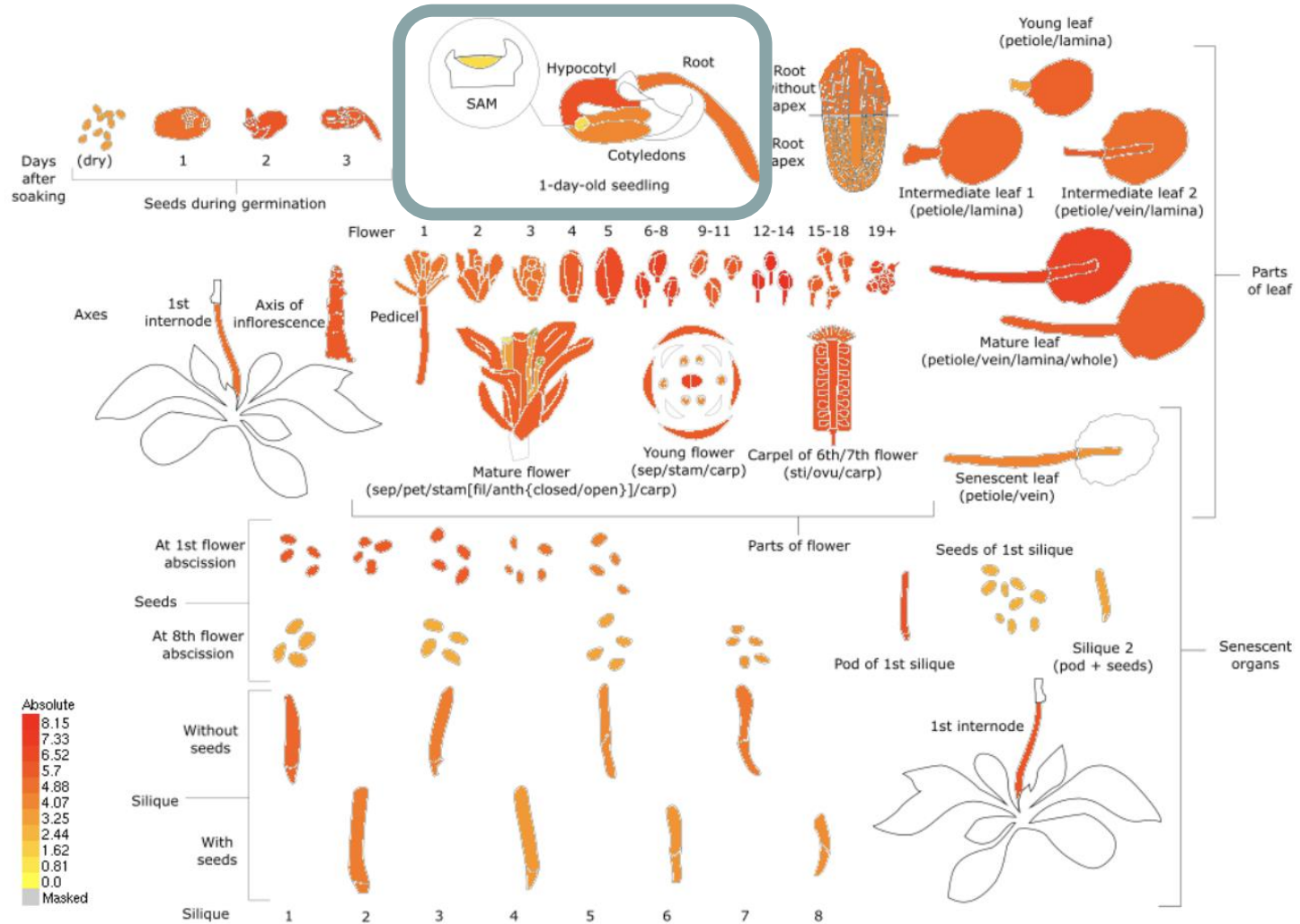
- (A) Dark-grown, wild-type seedlings; (B) light-grown, wild-type seedlings;  
(C) dark-grown *copl-1* seedlings; (D) light-grown *copl-1* seedlings.

# Annotation of *AtCOP1* (TAIR)

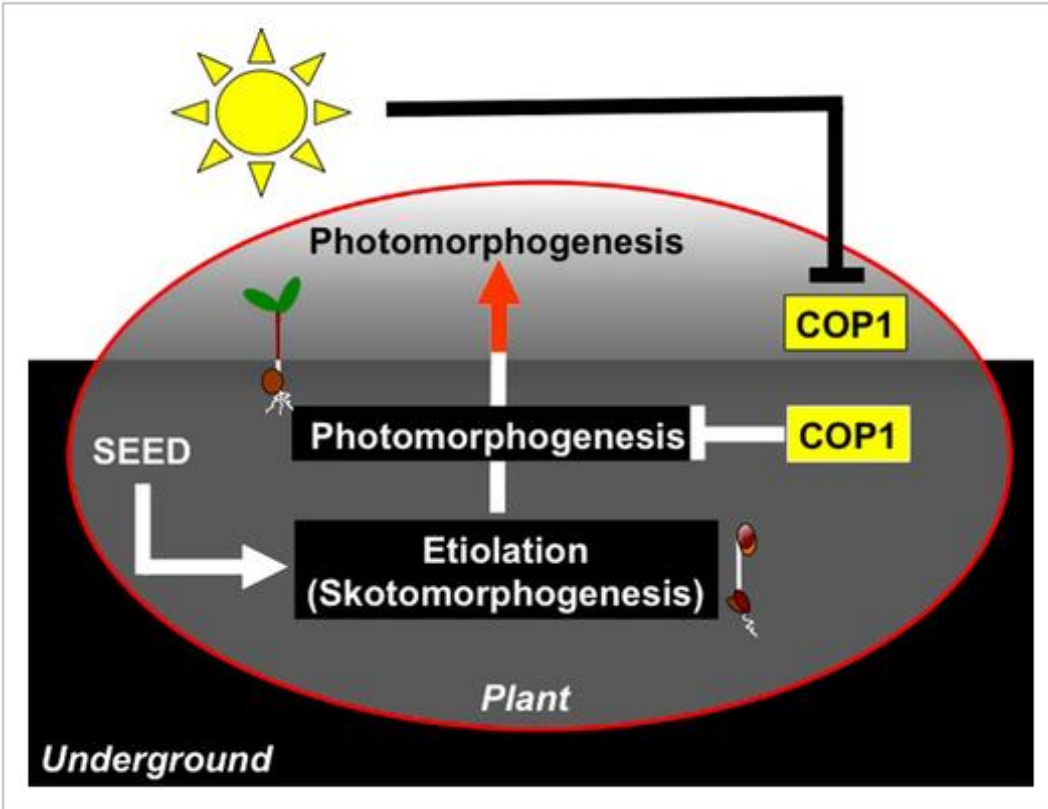


- Gene Locus: AT2G32950
- Extron: 13
- Intron: 12
- Alternative Splicing Form: 1
- GO Biological Process: photomorphogenesis, skotomorphogenesis, entrainment of circadian clock, photoperiodism, flowering, protein ubiquitination, regulation of stomatal movement, shade avoidance and so on.

# The expression pattern of *COP1* in *Arabidopsis* developmental process



# Working model in plants



NLS (Nuclear localization sequence)

120-177aa



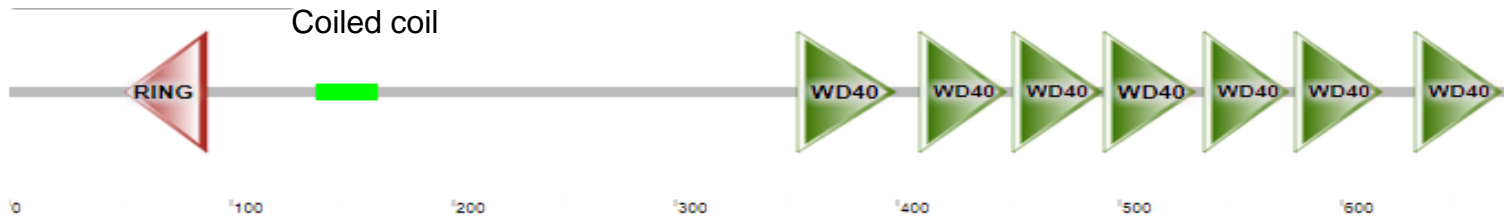
CLS (Cytoplasmic localization sequence)

67-177aa



(Emilio J. Sanchez-Barcelo, et al., Journal of Pineal Research, 2016)

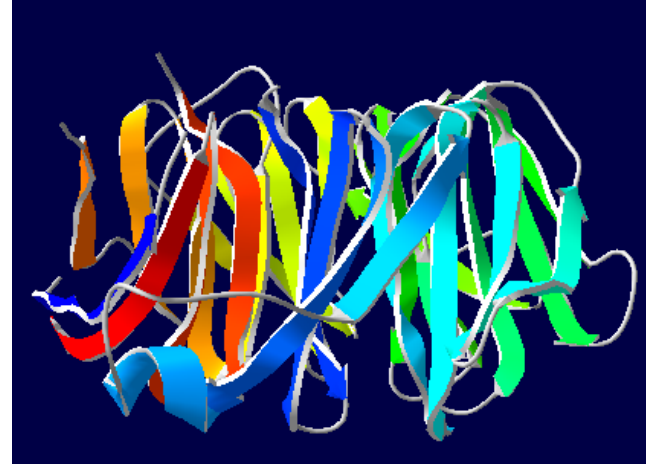
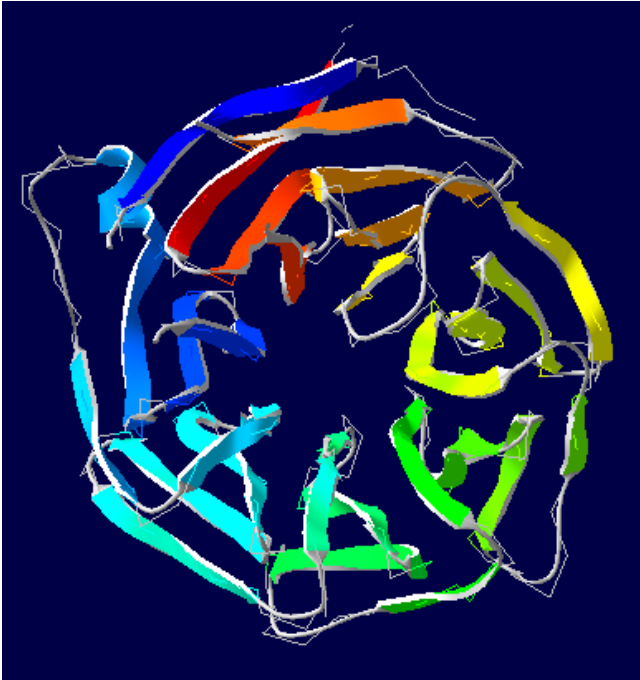
# Structure analysis of COP1 (SMART)



Name	Start	End	Function
RING	52	89	DNA or RNA binding, protein-protein interactions and membrane association.
Coiled coil	138	166	Scaffold to form thick bundles of fibres.
WD40-1	355	399	
WD40-2	410	449	Involved in cell division, mRNA modification,
WD40-3	452	492	transmembrane signal transduction, material
WD40-4	493	534	transport, and protein-protein interactions.
WD40-5	538	576	
WD40-6	579	618	
WD40-7	633	672	



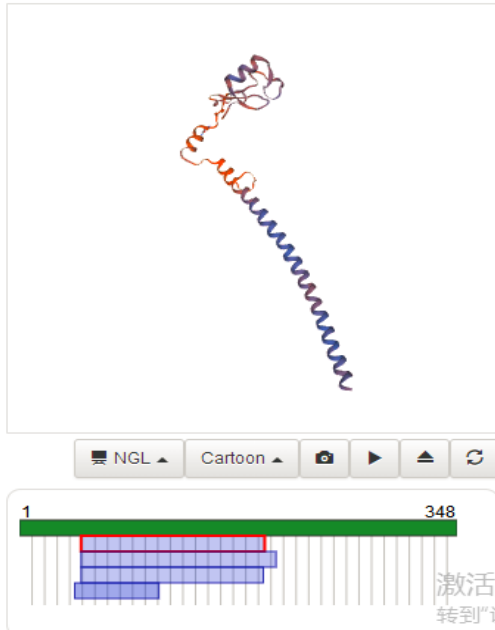
# Structure of AtCOP1 WD40: seven-bladed $\beta$ -propellers



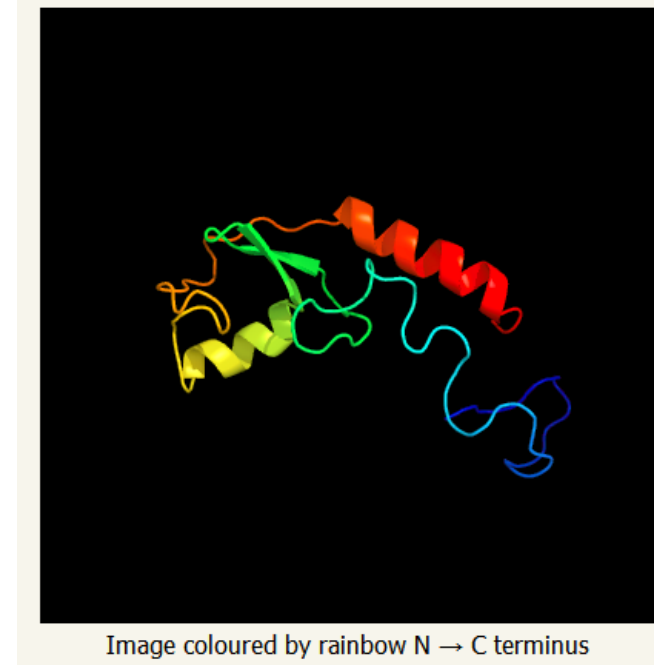
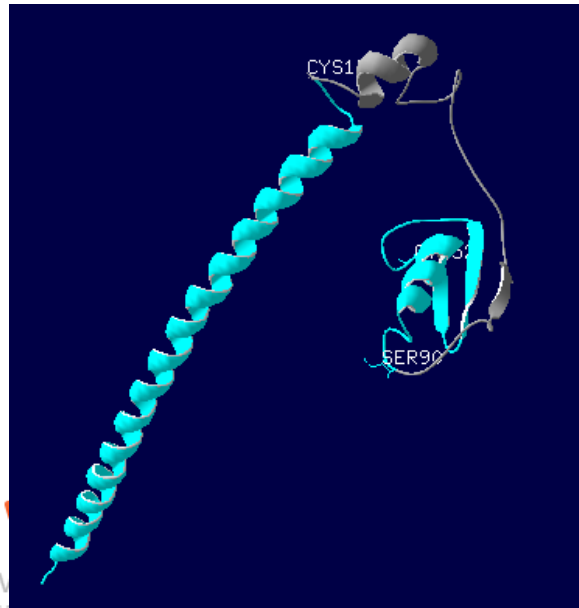
## Domains and Repeats

Feature key	Position(s)	Description
Repeat <sup>1</sup>	369 – 408	WD 1 <a href="#">↕ Sequence analysis</a>
Repeat <sup>1</sup>	418 – 458	WD 2 <a href="#">↕ Sequence analysis</a>
Repeat <sup>1</sup>	461 – 501	WD 3 <a href="#">↕ Sequence analysis</a>
Repeat <sup>1</sup>	503 – 543	WD 4 <a href="#">↕ Sequence analysis</a>
Repeat <sup>1</sup>	547 – 585	WD 5 <a href="#">↕ Sequence analysis</a>
Repeat <sup>1</sup>	588 – 627	WD 6 <a href="#">↕ Sequence analysis</a>
Repeat <sup>1</sup>	642 – 674	WD 7 <a href="#">↕ Sequence analysis</a>

# Structure model of AtCOP1 (1-348aa)

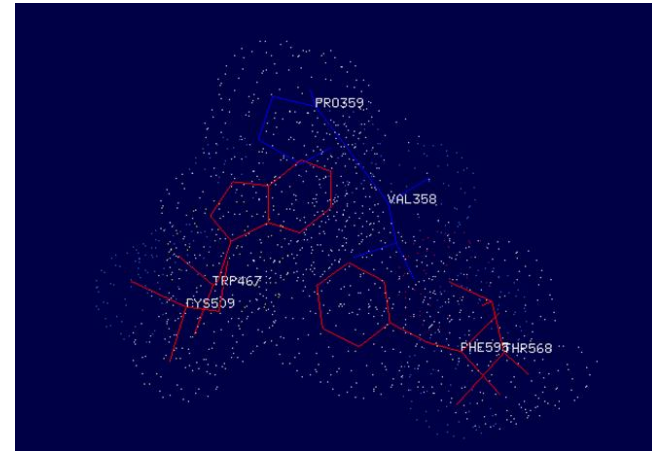
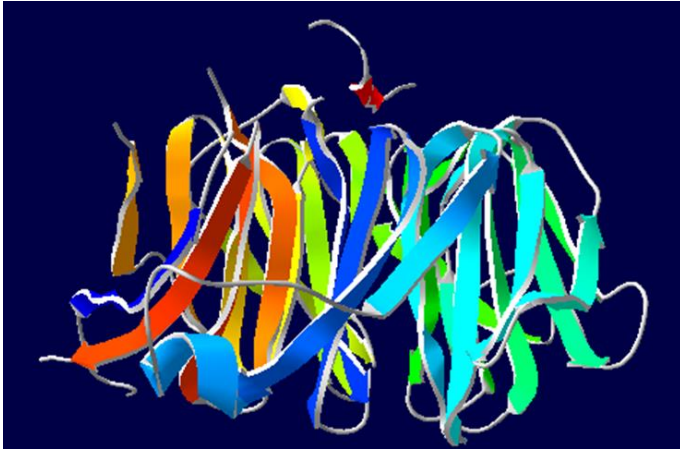


Swiss model: [5gmk.1.Z](#)

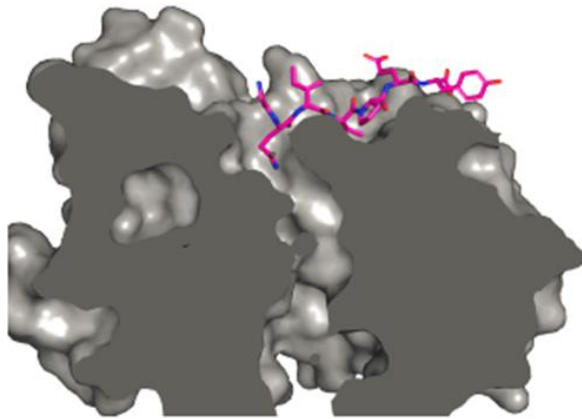


Phyre2: [c2kreA](#)

# HY5 and Trib1 bind to a highly conserved surface of the $\beta$ -propellers

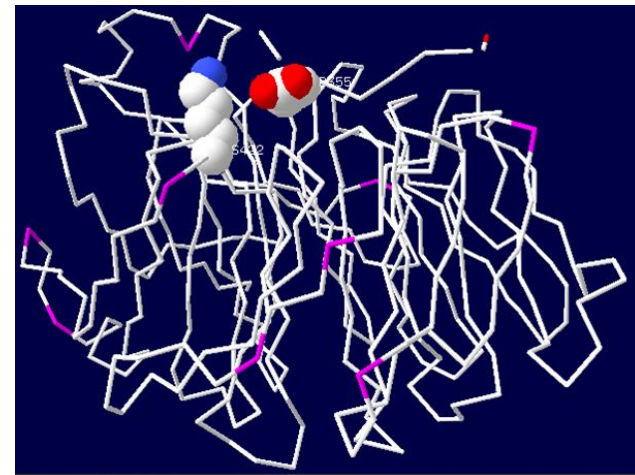


COP1:F595,T568,C509,W467,F595 Trib1: V358,P359



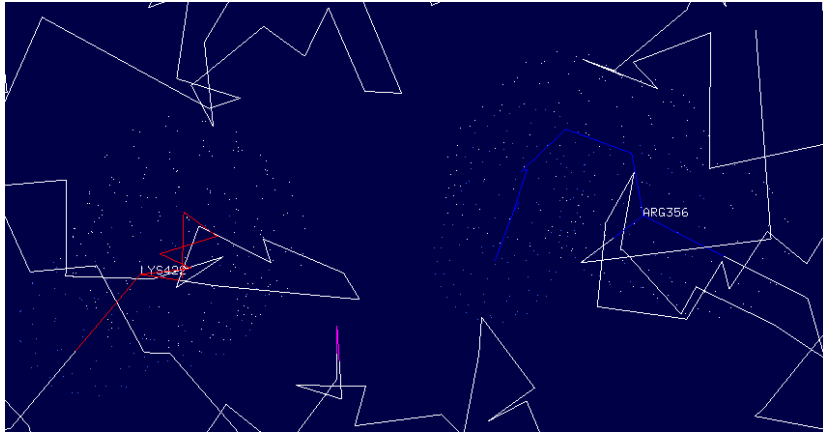
COP1/Trib1

(Sacha Uljon, et al., Structure, 2016)

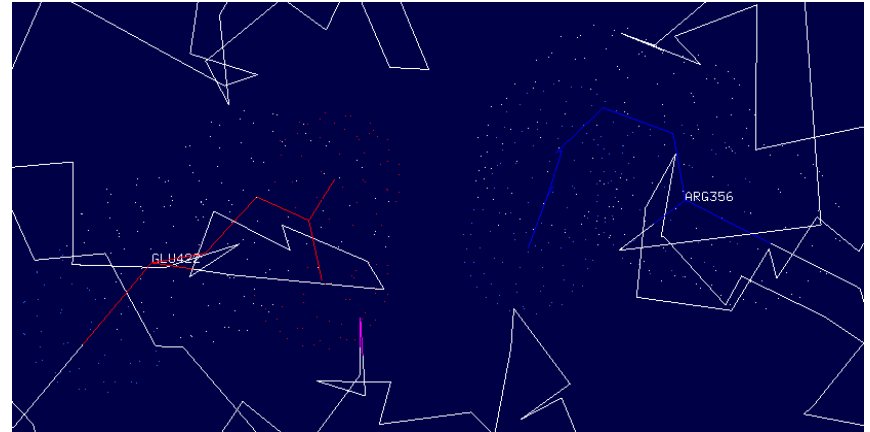


COP1:K422 Trib1:D355

# AtCOP1 WD40 K422E increases interaction between R356 of HY5

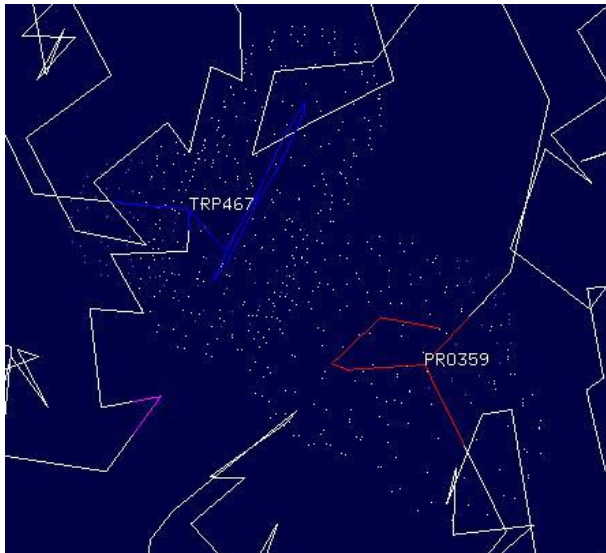


K422

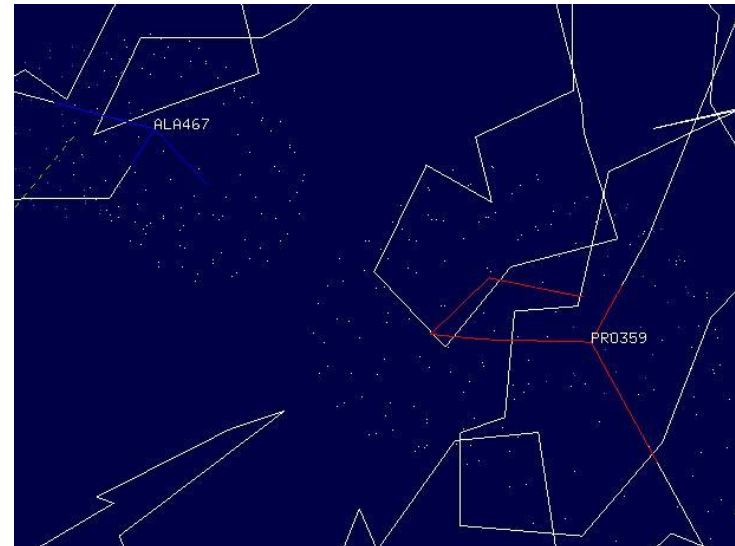


K422A

# AtCOP1 WD40 W467A decreases interaction between Pro359 of HY5

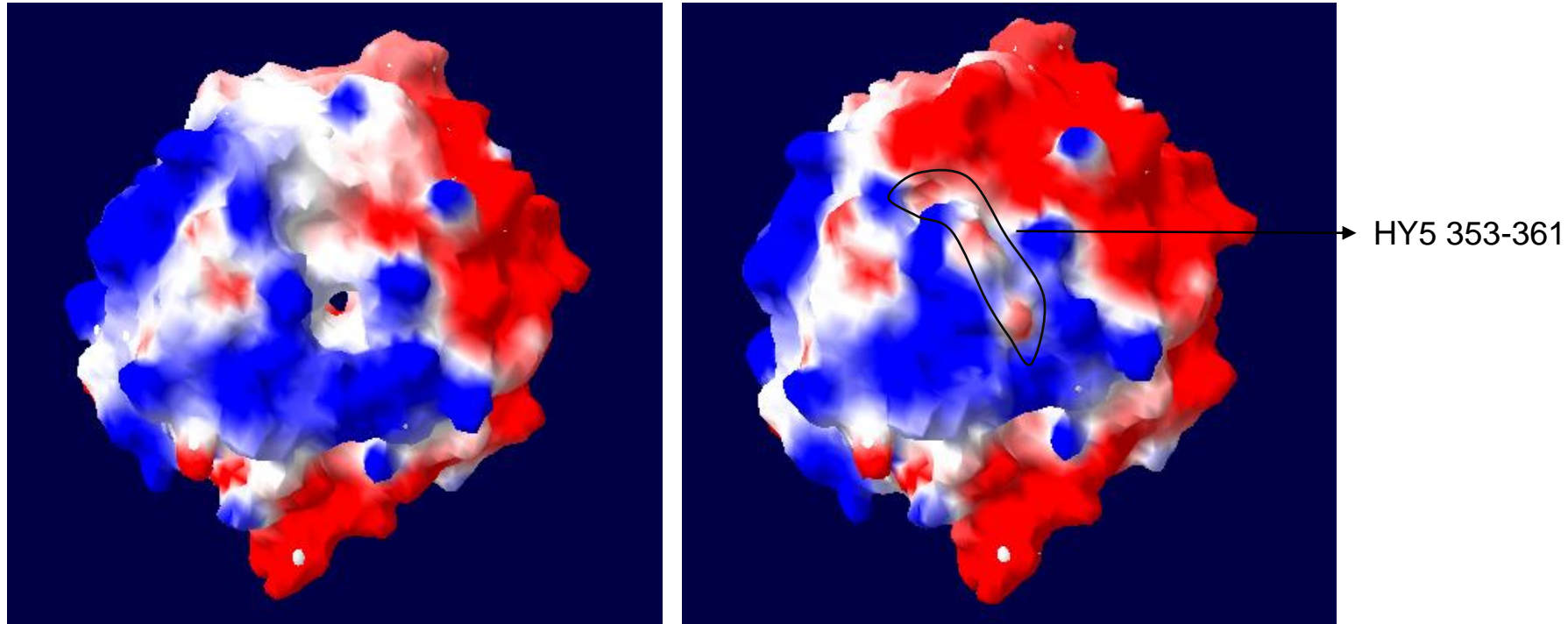


W467



W467A

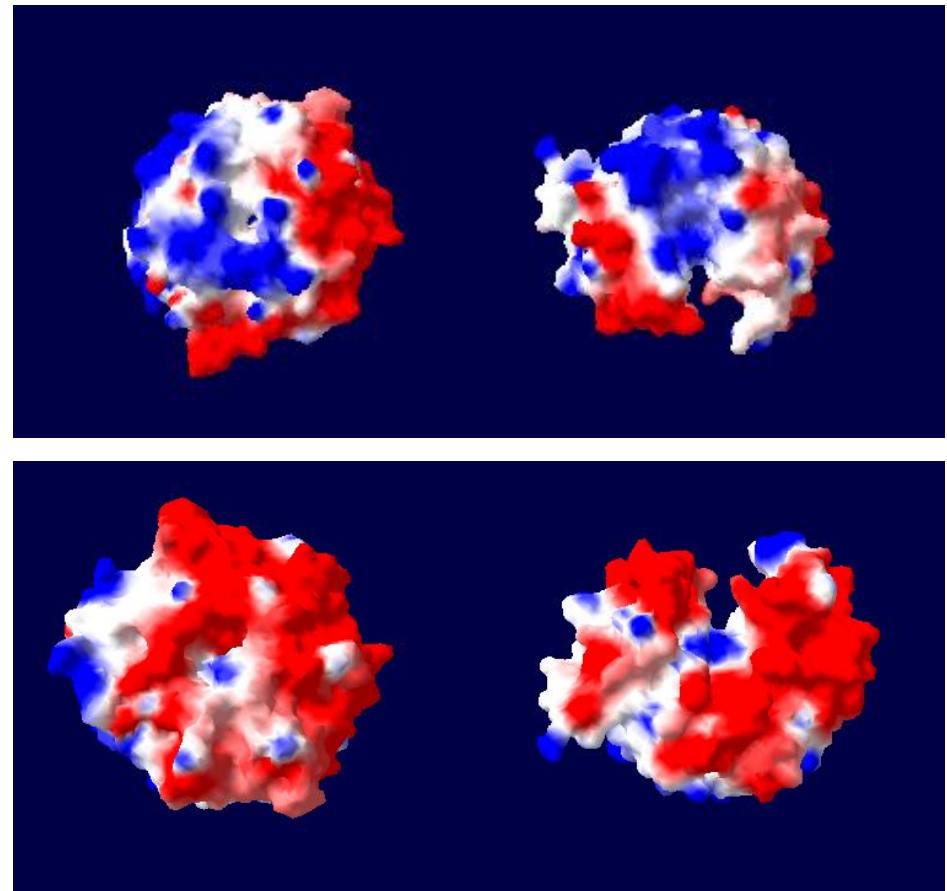
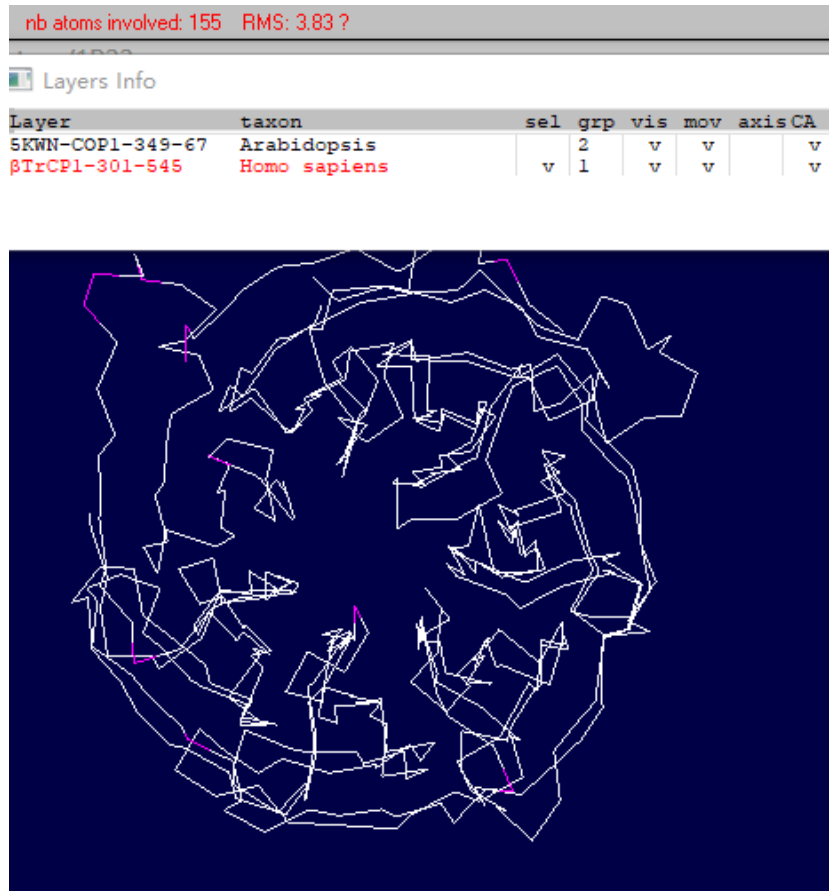
# AtCOP1 WD40 interacts with HY5 mainly through electrostatic interaction



Molecular surface of AtCOP1 WD40

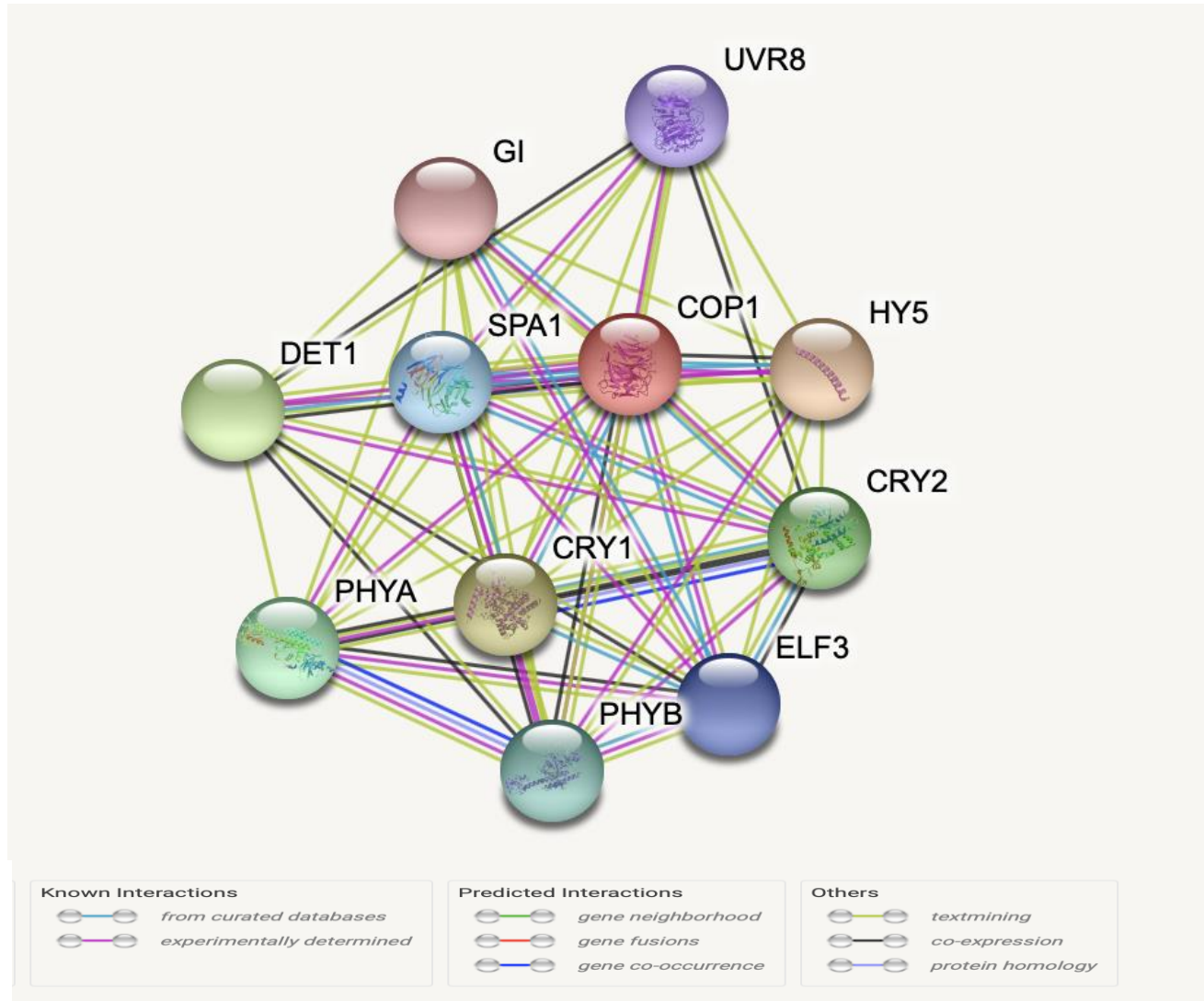
 Negative  
 Positive

WD40 may interact with other protein by the charged amino acids on the top/bottom surface of the  $\beta$ -propellers





# STRING analysis of AtCOP1 interaction



# STRING analysis of AtCOP1 interaction

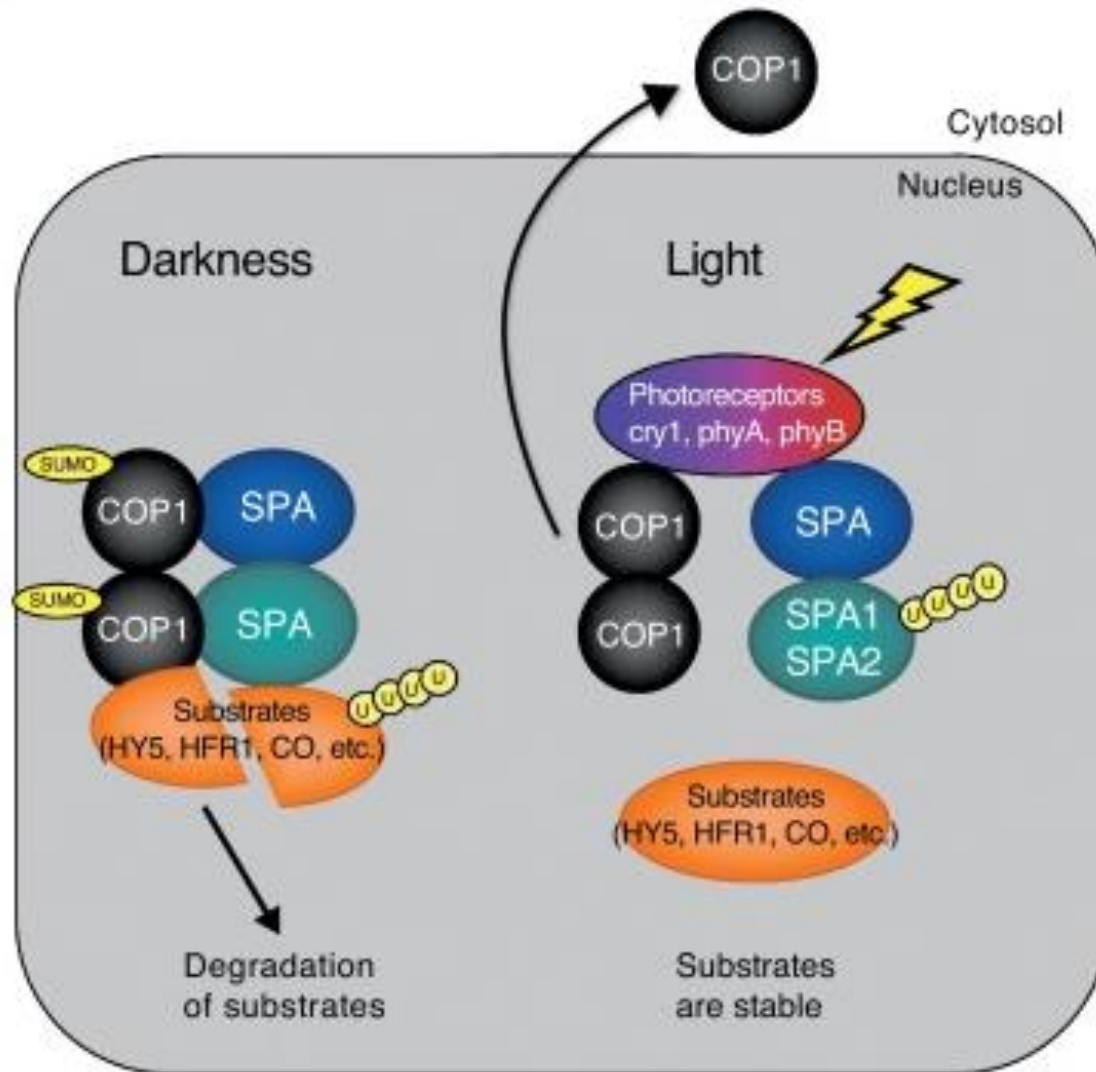
## Predicted Functional Partners:

		Neig	Gen	Co	Co	Expe	Data	Text	[/Hor	Scor
●	HY5	<i>ELONGATED HYPOCOTYL 5; Transcription factor that promotes photomorphogenesis in light. Acts downstream of the light...</i>				●	●	●		0.999
●	CRY1	<i>Cryptochrome 1; Photoreceptor that mediates primarily blue light inhibition of hypocotyl elongation and photoperiodic cont...</i>					●	●	●	0.997
●	DET1	<i>DE-ETIOLATED 1; Component of light signal transduction machinery. Involved in repression of photomorphogenesis in dark...</i>				●	●	●		0.996
●	CRY2	<i>Cryptochrome 2; Photoreceptor that mediates primarily blue light inhibition of hypocotyl elongation and photoperiodic cont...</i>					●	●	●	0.993
●	PHYA	<i>Phytochrome A; Regulatory photoreceptor which exists in two forms that are reversibly interconvertible by light- the Pr form...</i>					●		●	0.989
●	PHYB	<i>Phytochrome B; Regulatory photoreceptor which exists in two forms that are reversibly interconvertible by light- the Pr form...</i>				●	●		●	0.985
●	SPA1	<i>SUPPRESSOR OF PHYA-105 1; Controls normal photoperiodic flowering and regulates circadian rhythms. Required for supp...</i>				●	●	●	●	0.983
●	ELF3	<i>EARLY FLOWERING 3; May be a transcription factor part of a circadian clock input pathway. Acts within a 'zeitnehmer' feed...</i>					●	●	●	0.982
●	UVR8	<i>UVB-RESISTANCE 8; UV-B specific signaling component that acts as UV-B photoreceptor and plays a key role in establishin...</i>					●		●	0.976
●	GI	<i>GIGANTEA; Involved in regulation of circadian rhythm and photoperiodic flowering. May play a role in maintenance of circa...</i>					●	●	●	0.975

- Transcription factors: HY5   ELF3
- Receptors: CRY1   CRY2   PHYA   PHYB
- The other: DET1

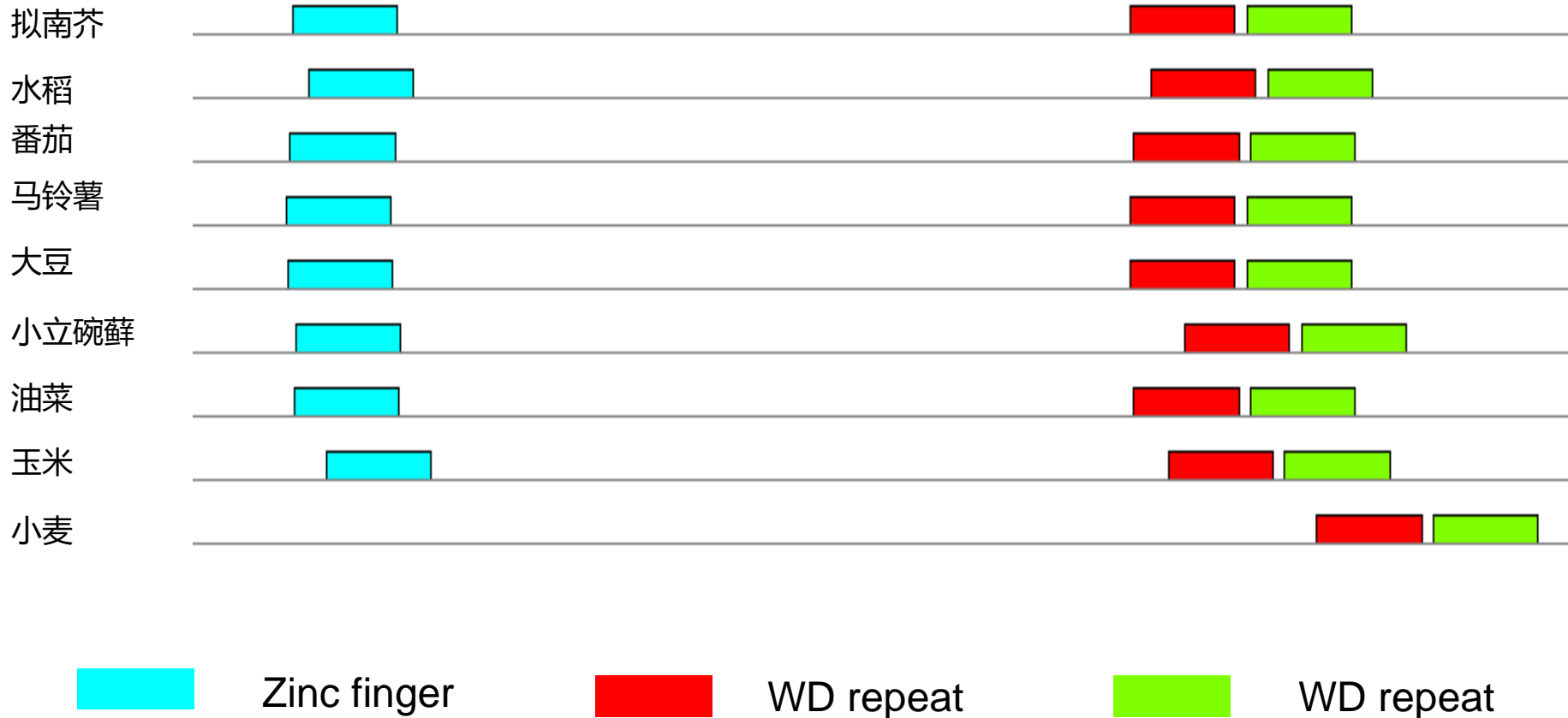


# The substrates of *COP1* in plants



(Hoecker U, et al., Curr Opin Plant Biol, 2017)

# Conserved motifs analysis (MEME)



# Conservative analysis (Weblogo)

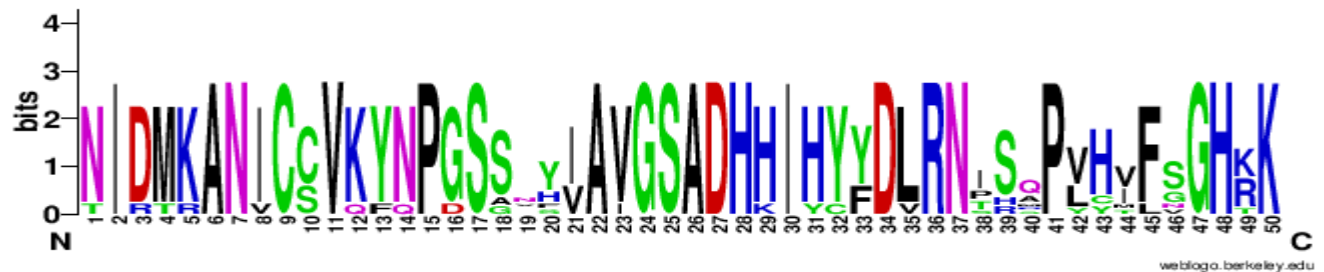
Motif1  
52aa-101aa



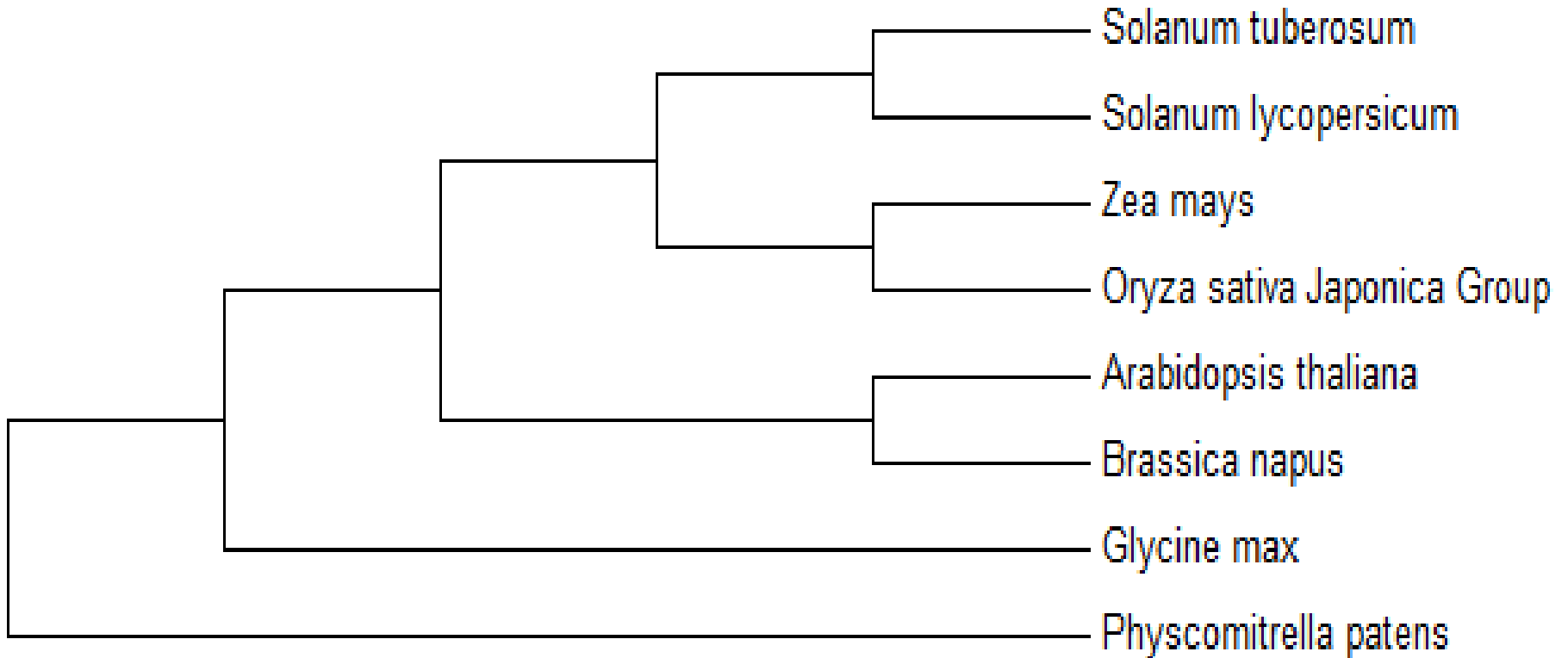
Motif2  
446aa-495aa



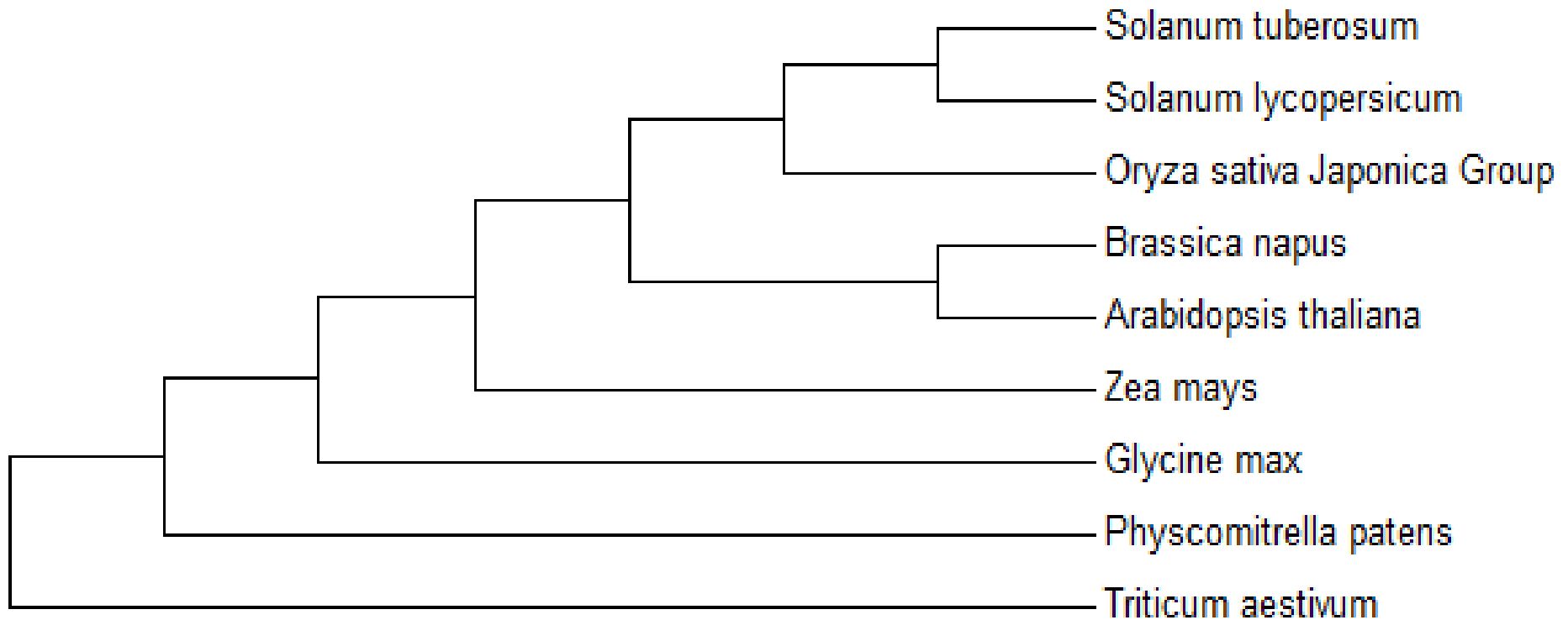
Motif3  
501aa-550aa



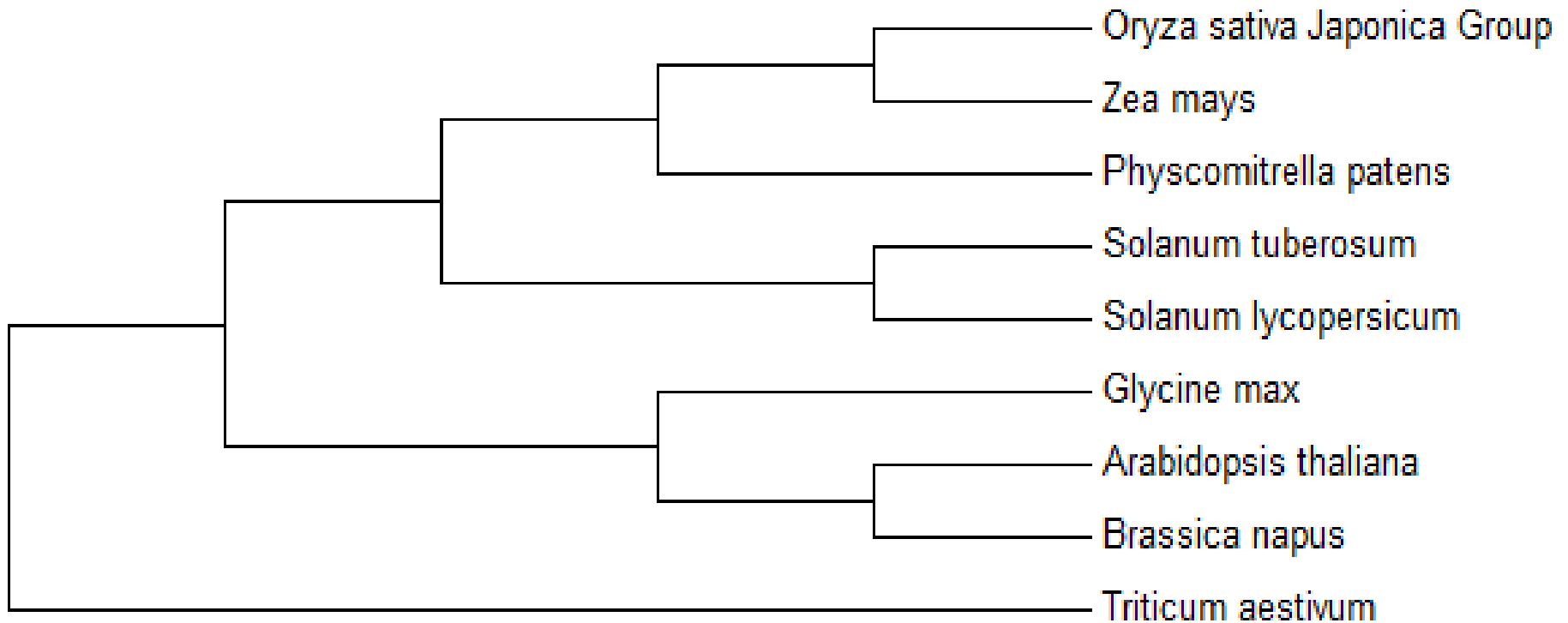
# Phylogeny analysis of motif1



# Phylogeny analysis of motif2



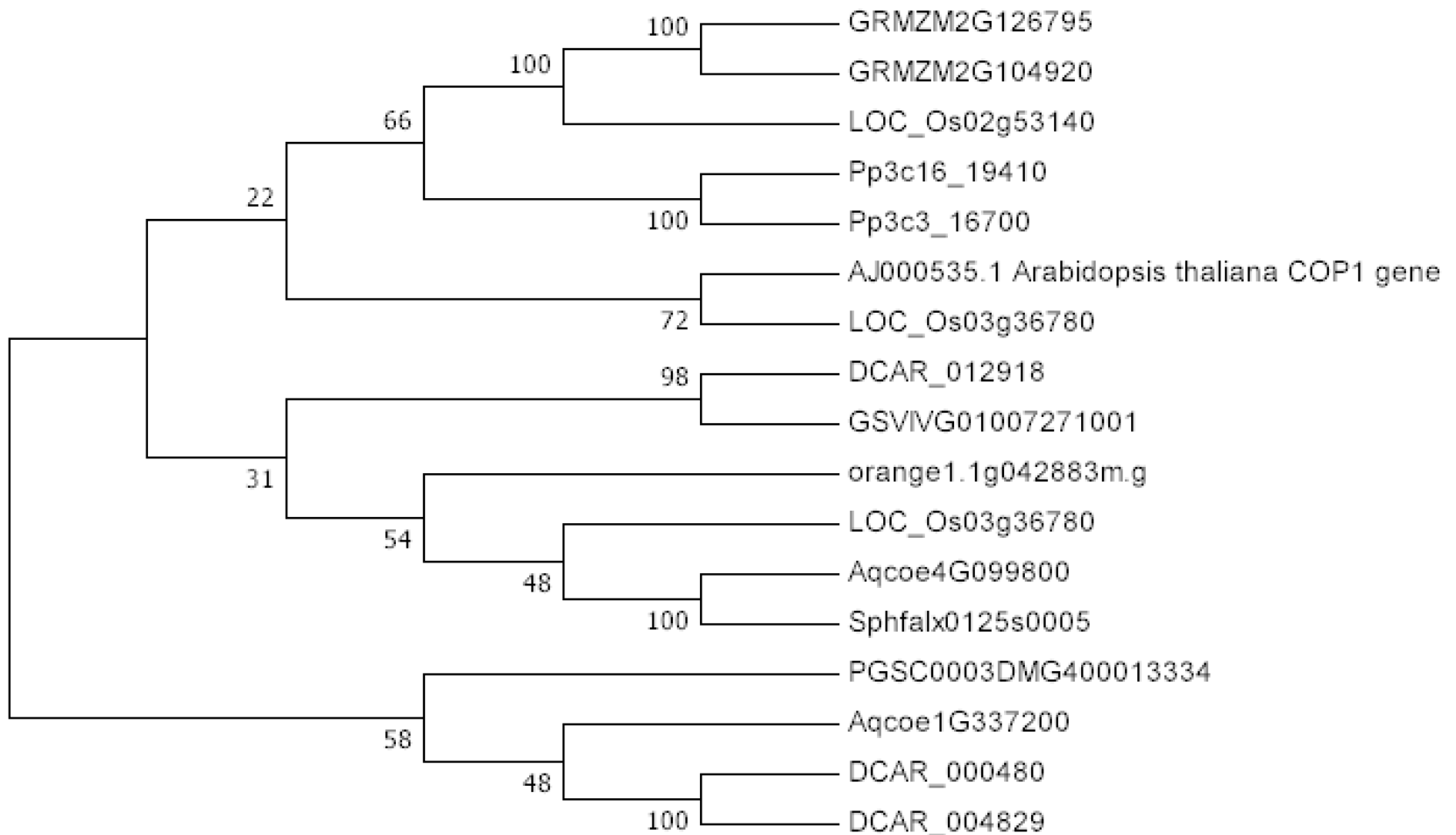
# Phylogeny analysis of motif3



# Homologous sequences in various species

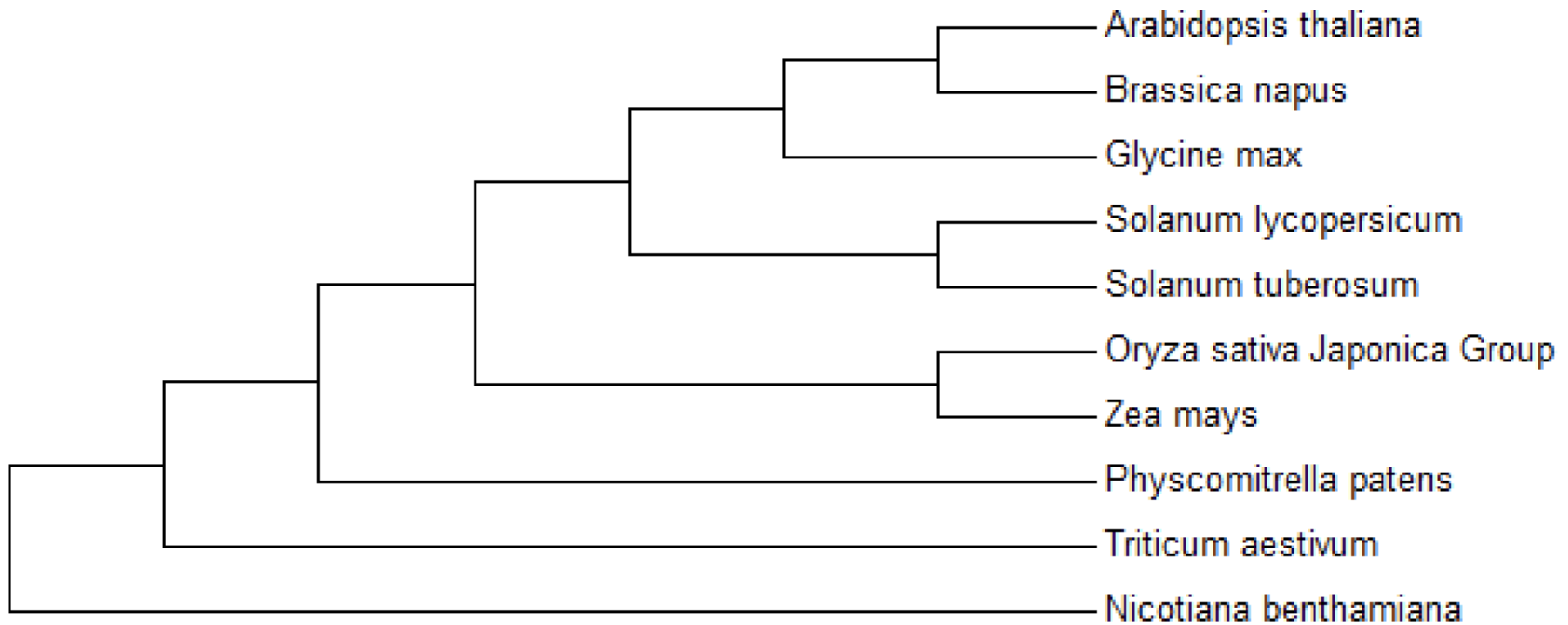
No.	Species	Gene ID	Sequence length	Protein Length
1	<i>Arabidopsis thaliana</i>	817857	6.9Kbp	675aa
2	<i>Solanum lycopersicum</i>	543547	14Kbp	677aa
3	<i>Homo sapiens</i>	64326	317Kbp	731aa
4	<i>Mus musculus</i>	26374	148Kbp	733aa
5	<i>Rattus norvegicus</i>	360860	113Kbp	733aa
6	<i>Danio rerio</i>	100037391	26Kbp	694aa
7	<i>Oryctolagus cuniculus</i>	100356568	252Kbp	627aa
8	<i>Macaca mulatta</i>	708802	309Kbp	731aa
9	<i>Pongo abelii</i>	100447738	315Kbp	731aa

# Phylogeny analysis of COP1 in plants (genomic sequence)

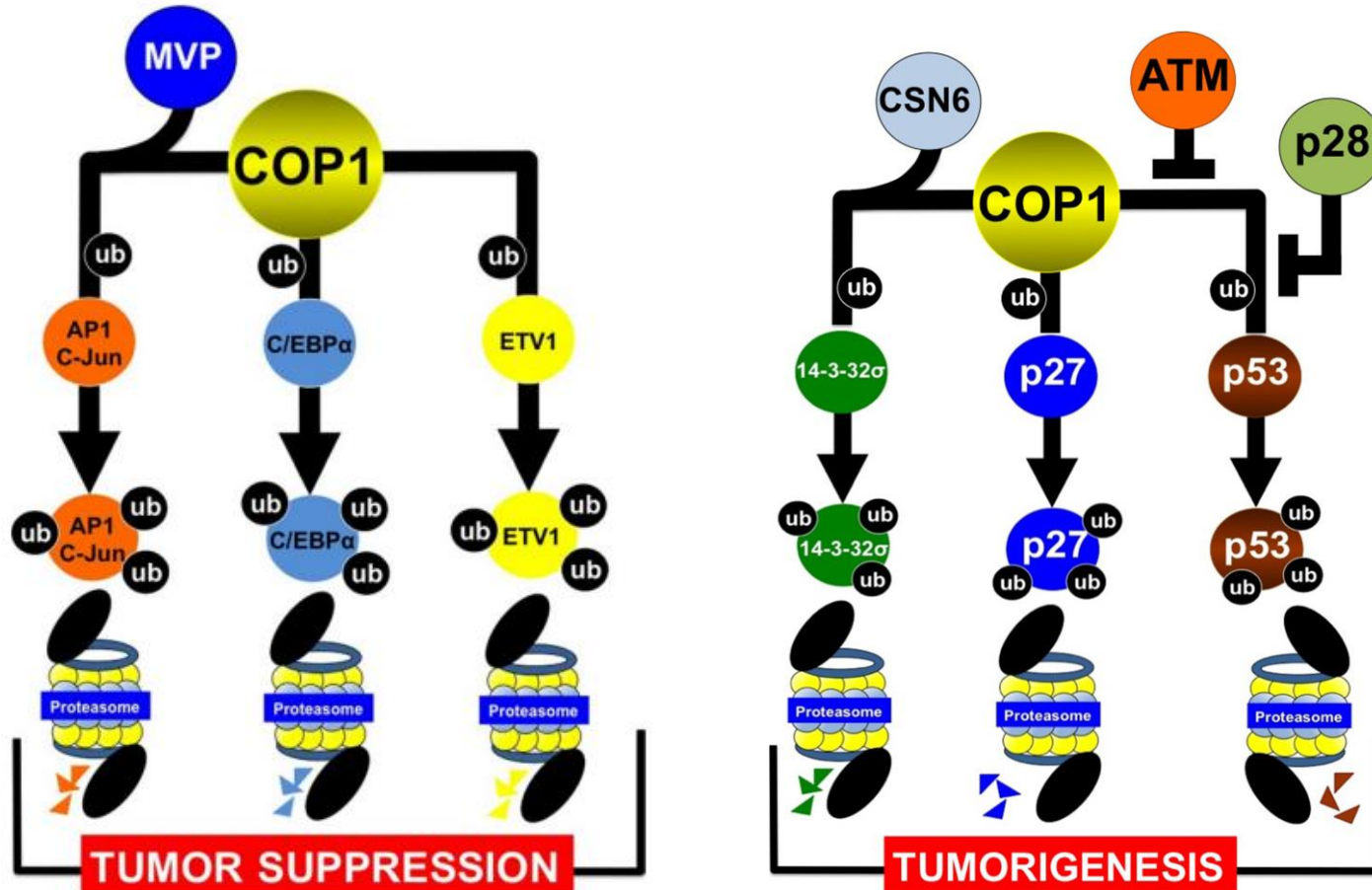




# Phylogeny analysis of COP1 in plants (protein sequence)



# *mCOP1* plays an important roles in mammalian



(Emilio J. Sanchez-Barcelo, et al., Journal of Pineal Research, 2016)

# Function of COP1 between animals and plants

**FEEDING-TO-FASTING  
TRANSITION**  
(Inhibition of gluconeogenesis and lipogenesis; activation of lipolysis)



**DARK-TO-LIGHT  
TRANSITION**  
From etiolation to photosynthesis

(Emilio J. Sanchez-Barcelo, et al., Journal of Pineal Research, 2016)

THANKS!

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